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Sequence Listing was accepted.
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Reviewer: Anne Corrigan
Timestamp: [year=2008; month=7; day=21; hr=13; min=42; sec=21; ms=289; ]
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<110> BATTINI, JEAN-LUC GEORGES LAURENT

      MANEL, NICOLAS GABRIEL ALBERT

      KIM, FELIX JINHYUN

      KINET, SANDRINA

      TAYLOR, NAOMI

      SITBON, MARC

<120> GLUT-1 AS A RECEPTOR FOR HTLV ENVELOPES AND ITS USES

<130> 0508-1149

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<150> PCT/EP2004/004624
<151> 2004-04-30

<150> EP 03291067.1
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Met Glu Pro Ser Ser Lys Lys Leu Thr Gly Arg Leu Met Leu Ala Val
 1           5              10              15

gga gga gca gtg ctt ggc tcc ctg cag ttt ggc tac aac act gga gtc   96
Gly Gly Ala Val Leu Gly Ser Leu Gln Phe Gly Tyr Asn Thr Gly Val
          20              25              30

atc aat gcc ccc cag aag gtg atc gag gag ttc tac aac cag aca tgg  144
Ile Asn Ala Pro Gln Lys Val Ile Glu Glu Phe Tyr Asn Gln Thr Trp
        35            40              45

gtc cac cgc tat ggg gag agc atc ctg ccc acc acg ctc acc acg ctc  192
Val His Arg Tyr Gly Glu Ser Ile Leu Pro Thr Thr Leu Thr Thr Leu
    50            55            60

tgg tcc ctc tca gtg gcc atc ttt tct gtt ggg ggc atg att ggc tcc  240
Trp Ser Leu Ser Val Ala Ile Phe Ser Val Gly Gly Met Ile Gly Ser
 65           70           75          80

ttc tct gtg ggc ctt ttc gtt aac cgc ttt ggc cgg cgg aat tca atg    288
Phe Ser Val Gly Leu Phe Val Asn Arg Phe Gly Arg Arg Asn Ser Met
                85                  90                  95

ctg atg atg aac ctg ctg gcc ttc gtg tcc gcc gtg ctc atg ggc ttc    336
Leu Met Met Asn Leu Leu Ala Phe Val Ser Ala Val Leu Met Gly Phe
            100                 105                 110

tcg aaa ctg ggc aag tcc ttt gag atg ctg atc ctg ggc cgc ttc atc    384
Ser Lys Leu Gly Lys Ser Phe Glu Met Leu Ile Leu Gly Arg Phe Ile
        115                 120                 125

atc ggt gtg tac tgc ggc ctg acc aca ggc ttc gtg ccc atg tat gtg    432
Ile Gly Val Tyr Cys Gly Leu Thr Thr Gly Phe Val Pro Met Tyr Val
    130                 135                 140

ggt gaa gtg tca ccc aca gcc ttt cgt ggg gcc ctg ggc acc ctg cac    480
Gly Glu Val Ser Pro Thr Ala Phe Arg Gly Ala Leu Gly Thr Leu His
145                 150                 155                 160

cag ctg ggc atc gtc gtc ggc atc ctc atc gcc cag gtg ttc ggc ctg    528
Gln Leu Gly Ile Val Val Gly Ile Leu Ile Ala Gln Val Phe Gly Leu
                165                 170                 175

gac tcc atc atg ggc aac aag gac ctg tgg ccc ctg ctg ctg agc atc    576
Asp Ser Ile Met Gly Asn Lys Asp Leu Trp Pro Leu Leu Leu Ser Ile
            180                 185                 190

atc ttc atc ccg gcc ctg ctg cag tgc atc gtg ctg ccc ttc tgc ccc    624
Ile Phe Ile Pro Ala Leu Leu Gln Cys Ile Val Leu Pro Phe Cys Pro
        195                 200                 205

gag agt ccc cgc ttc ctg ctc atc aac cgc aac gag gag aac cgg gcc    672
Glu Ser Pro Arg Phe Leu Leu Ile Asn Arg Asn Glu Glu Asn Arg Ala
    210                 215                 220

aag agt gtg cta aag aag ctg cgc ggg aca gct gac gtg acc cat gac    720
Lys Ser Val Leu Lys Lys Leu Arg Gly Thr Ala Asp Val Thr His Asp
225                 230                 235                 240

ctg cag gag atg aag gaa gag agt cgg cag atg atg cgg gag aag aag    768
Leu Gln Glu Met Lys Glu Glu Ser Arg Gln Met Met Arg Glu Lys Lys
                245                 250                 255

gtc acc atc ctg gag ctg ttc cgc tcc ccc gcc tac cgc cag ccc atc    816
Val Thr Ile Leu Glu Leu Phe Arg Ser Pro Ala Tyr Arg Gln Pro Ile
            260                 265                 270

ctc atc gct gtg gtg ctg cag ctg tcc cag cag ctg tct ggc atc aac    864
Leu Ile Ala Val Val Leu Gln Leu Ser Gln Gln Leu Ser Gly Ile Asn
        275                 280                 285

gct gtc ttc tat tac tcc acg agc atc ttc gag aag gcg ggg gtg cag    912
Ala Val Phe Tyr Tyr Ser Thr Ser Ile Phe Glu Lys Ala Gly Val Gln
    290                 295                 300

cag cct gtg tat gcc acc att ggc tcc ggt atc gtc aac acg gcc ttc    960

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Gln Pro Val Tyr Ala Thr Ile Gly Ser Gly Ile Val Asn Thr Ala Phe
305                 310                 315                 320


act gtc gtg tcg ctg ttt gtg gtg gag cga gca ggc cgg cgg acc ctg      1008
Thr Val Val Ser Leu Phe Val Val Glu Arg Ala Gly Arg Arg Thr Leu
                325                 330                 335


cac ctc ata ggc ctc gct ggc atg gcg ggt tgt gcc ata ctc atg acc      1056
His Leu Ile Gly Leu Ala Gly Met Ala Gly Cys Ala Ile Leu Met Thr
                340                 345                 350


atc gcg cta gca ctg ctg gag cag cta ccc tgg atg tcc tat ctg agc      1104
Ile Ala Leu Ala Leu Leu Glu Gln Leu Pro Trp Met Ser Tyr Leu Ser
            355                 360                 365


atc gtg gcc atc ttt ggc ttt gtg gcc ttc ttt gaa gtg ggt cct ggc      1152
Ile Val Ala Ile Phe Gly Phe Val Ala Phe Phe Glu Val Gly Pro Gly
        370                 375                 380


ccc atc cca tgg ttc atc gtg gct gaa ctc ttc agc cag ggt cca cgt      1200
Pro Ile Pro Trp Phe Ile Val Ala Glu Leu Phe Ser Gln Gly Pro Arg
385                 390                 395                 400


cca gct gcc att gcc gtt gca ggc ttc tcc aac tgg acc tca aat ttc      1248
Pro Ala Ala Ile Ala Val Ala Gly Phe Ser Asn Trp Thr Ser Asn Phe
                405                 410                 415


att gtg ggc atg tgc ttc cag tat gtg gag caa ctg tgt ggt ccc tac      1296
Ile Val Gly Met Cys Phe Gln Tyr Val Glu Gln Leu Cys Gly Pro Tyr
                420                 425                 430


gtc ttc atc atc ttc act gtg ctc ctg gtt ctg ttc ttc atc ttc acc      1344
Val Phe Ile Ile Phe Thr Val Leu Leu Val Leu Phe Phe Ile Phe Thr
            435                 440                 445


tac ttc aaa gtt cct gag act aaa ggc cgg acc ttc gat gag atc gct      1392
Tyr Phe Lys Val Pro Glu Thr Lys Gly Arg Thr Phe Asp Glu Ile Ala
        450                 455                 460


tcc ggc ttc cgg cag ggg gga gcc agc caa agt gat aag aca ccc gag      1440
Ser Gly Phe Arg Gln Gly Gly Ala Ser Gln Ser Asp Lys Thr Pro Glu
465                 470                 475                 480


gag ctg ttc cat ccc ctg ggg gct gat tcc caa gtg tga               1479
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<211> 492
<212> PRT
<213> Homo sapiens

<400> 2
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Gly Gly Ala Val Leu Gly Ser Leu Gln Phe Gly Tyr Asn Thr Gly Val
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Ile Asn Ala Pro Gln Lys Val Ile Glu Glu Phe Tyr Asn Gln Thr Trp
          35                  40                  45

Val His Arg Tyr Gly Glu Ser Ile Leu Pro Thr Thr Leu Thr Thr Leu
          50                  55                  60

Trp Ser Leu Ser Val Ala Ile Phe Ser Val Gly Gly Met Ile Gly Ser
65                  70                  75                  80

Phe Ser Val Gly Leu Phe Val Asn Arg Phe Gly Arg Arg Asn Ser Met
                  85                  90                  95

Leu Met Met Asn Leu Leu Ala Phe Val Ser Ala Val Leu Met Gly Phe
          100                 105                 110

Ser Lys Leu Gly Lys Ser Phe Glu Met Leu Ile Leu Gly Arg Phe Ile
          115                 120                 125

Ile Gly Val Tyr Cys Gly Leu Thr Thr Gly Phe Val Pro Met Tyr Val
          130                 135                 140

Gly Glu Val Ser Pro Thr Ala Phe Arg Gly Ala Leu Gly Thr Leu His
145                 150                 155                 160

Gln Leu Gly Ile Val Val Gly Ile Leu Ile Ala Gln Val Phe Gly Leu
                  165                 170                 175

Asp Ser Ile Met Gly Asn Lys Asp Leu Trp Pro Leu Leu Leu Ser Ile
          180                 185                 190

Ile Phe Ile Pro Ala Leu Leu Gln Cys Ile Val Leu Pro Phe Cys Pro
          195                 200                 205

Glu Ser Pro Arg Phe Leu Leu Ile Asn Arg Asn Glu Glu Asn Arg Ala
          210                 215                 220

Lys Ser Val Leu Lys Lys Leu Arg Gly Thr Ala Asp Val Thr His Asp
225                 230                 235                 240

Leu Gln Glu Met Lys Glu Glu Ser Arg Gln Met Met Arg Glu Lys Lys
                  245                 250                 255

Val Thr Ile Leu Glu Leu Phe Arg Ser Pro Ala Tyr Arg Gln Pro Ile
          260                 265                 270

Leu Ile Ala Val Val Leu Gln Leu Ser Gln Gln Leu Ser Gly Ile Asn
          275                 280                 285

Ala Val Phe Tyr Tyr Ser Thr Ser Ile Phe Glu Lys Ala Gly Val Gln
          290                 295                 300

Gln Pro Val Tyr Ala Thr Ile Gly Ser Gly Ile Val Asn Thr Ala Phe
305                 310                 315                 320

Thr Val Val Ser Leu Phe Val Val Glu Arg Ala Gly Arg Arg Thr Leu
          325                 330                 335

His Leu Ile Gly Leu Ala Gly Met Ala Gly Cys Ala Ile Leu Met Thr
          340                 345                 350

Ile Ala Leu Ala Leu Leu Glu Gln Leu Pro Trp Met Ser Tyr Leu Ser
          355                 360                 365

Ile Val Ala Ile Phe Gly Phe Val Ala Phe Phe Glu Val Gly Pro Gly
          370                 375                 380

Pro Ile Pro Trp Phe Ile Val Ala Glu Leu Phe Ser Gln Gly Pro Arg
385                 390                 395                 400

Pro Ala Ala Ile Ala Val Ala Gly Phe Ser Asn Trp Thr Ser Asn Phe
          405                 410                 415

Ile Val Gly Met Cys Phe Gln Tyr Val Glu Gln Leu Cys Gly Pro Tyr
          420                 425                 430

Val Phe Ile Ile Phe Thr Val Leu Leu Val Leu Phe Phe Ile Phe Thr
          435                 440                 445

Tyr Phe Lys Val Pro Glu Thr Lys Gly Arg Thr Phe Asp Glu Ile Ala
          450                 455                 460

Ser Gly Phe Arg Gln Gly Gly Ala Ser Gln Ser Asp Lys Thr Pro Glu
465                 470                 475                 480

Glu Leu Phe His Pro Leu Gly Ala Asp Ser Gln Val
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<212> DNA
<213> Human T-cell lymphotropic virus type 1

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<221> CDS
<222> (1)..(924)

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  1               5                  10                  15

ctc atc ctc ggt gat tac agc ccc agc tgc tgt act ctc aca att gga    96
Leu Ile Leu Gly Asp Tyr Ser Pro Ser Cys Cys Thr Leu Thr Ile Gly
              20                  25                  30

gtc tcc tca tac cac tct aaa ccc tgc aat cct gcc cag cca gtt tgt    144
Val Ser Ser Tyr His Ser Lys Pro Cys Asn Pro Ala Gln Pro Val Cys
          35                  40                  45

tcg tgg acc ctc gac ctg ctg gcc ctt tca gcg gat cag gcc cta cag    192

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Ser Trp Thr Leu Asp Leu Leu Ala Leu Ser Ala Asp Gln Ala Leu Gln
     50                  55                  60


ccc ccc tgc cct aat cta gta agt tac tcc agc tac cat gcc acc tat      240
Pro Pro Cys Pro Asn Leu Val Ser Tyr Ser Ser Tyr His Ala Thr Tyr
 65                  70                  75                  80


tcc cta tat cta ttc cct cat tgg att aaa aag cca aac cga aat ggc      288
Ser Leu Tyr Leu Phe Pro His Trp Ile Lys Lys Pro Asn Arg Asn Gly
                 85                  90                  95


gga ggc tat tat tca gcc tct tat tca gac cct tgt tcc tta aag tgc      336
Gly Gly Tyr Tyr Ser Ala Ser Tyr Ser Asp Pro Cys Ser Leu Lys Cys
                100                 105                 110


cca tac ctg ggg tgc caa tca tgg acc tgc ccc tat aca gga gcc gtc      384
Pro Tyr Leu Gly Cys Gln Ser Trp Thr Cys Pro Tyr Thr Gly Ala Val
            115                 120                 125


tcc agc ccc tac tgg aag ttt cag caa gat gtc aat ttt act caa gaa      432
Ser Ser Pro Tyr Trp Lys Phe Gln Gln Asp Val Asn Phe Thr Gln Glu
        130                 135                 140


gtt tca cgc ctc aat att aat ctc cat ttt tca aaa tgc ggt ttt ccc      480
Val Ser Arg Leu Asn Ile Asn Leu His Phe Ser Lys Cys Gly Phe Pro
145                 150                 155                 160


ttc tcc ctt cta gtc gac gct cca gga tat gac ccc atc tgg ttc ctt      528
Phe Ser Leu Leu Val Asp Ala Pro Gly Tyr Asp Pro Ile Trp Phe Leu
                165                 170                 175


aat acc gaa ccc agc caa ctg cct ccc acc gcc cct cct cta ctc ccc      576
Asn Thr Glu Pro Ser Gln Leu Pro Pro Thr Ala Pro Pro Leu Leu Pro
                180                 185                 190


cac tct aac cta gac cac atc ctc gag ccc tct ata cca tgg aaa tca      624
His Ser Asn Leu Asp His Ile Leu Glu Pro Ser Ile Pro Trp Lys Ser
            195                 200                 205


aaa ctc ctg acc ctt gtc cag tta acc cta caa agc act aat tat act      672
Lys Leu Leu Thr Leu Val Gln Leu Thr Leu Gln Ser Thr Asn Tyr Thr
        210                 215                 220


tgc att gtc tgt atc gat cgt gcc agc cta tcc act tgg cac gtc cta      720
Cys Ile Val Cys Ile Asp Arg Ala Ser Leu Ser Thr Trp His Val Leu
225                 230                 235                 240


tac tct ccc aac gtc tct gtt cca tcc tct tct tct acc ccc ctc ctt      768
Tyr Ser Pro Asn Val Ser Val Pro Ser Ser Ser Ser Thr Pro Leu Leu
                245                 250                 255


tac cca tcg tta gcg ctt cca gcc ccc cac ctg acg tta cca ttt aac      816
Tyr Pro Ser Leu Ala Leu Pro Ala Pro His Leu Thr Leu Pro Phe Asn
                260                 265                 270


tgg acc cac tgc ttt gac ccc cag att caa gct ata gtc tcc tcc ccc      864
Trp Thr His Cys Phe Asp Pro Gln Ile Gln Ala Ile Val Ser Ser Pro
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tgt cat aac tcc ctc atc ctg ccc ccc ttt tcc ttg tca cct gtt ccc   912
Cys His Asn Ser Leu Ile Leu Pro Pro Phe Ser Leu Ser Pro Val Pro
290                 295                 300

acc cta gga tcc                                                   924
Thr Leu Gly Ser
305
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<212> PRT
<213> Human T-cell lymphotropic virus type 1

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Leu Ile Leu Gly Asp Tyr Ser Pro Ser Cys Cys Thr Leu Thr Ile Gly
              20                  25                  30

Val Ser Ser Tyr His Ser Lys Pro Cys Asn Pro Ala Gln Pro Val Cys
              35                  40                  45

Ser Trp Thr Leu Asp Leu Leu Ala Leu Ser Ala Asp Gln Ala Leu Gln
     50                  55                  60

Pro Pro Cys Pro Asn Leu Val Ser Tyr Ser Ser Tyr His Ala Thr Tyr
 65                  70                  75                  80

Ser Leu Tyr Leu Phe Pro His Trp Ile Lys Lys Pro Asn Arg Asn Gly
                 85                  90                  95

Gly Gly Tyr Tyr Ser Ala Ser Tyr Ser Asp Pro Cys Ser Leu Lys Cys
              100                 105                 110

Pro Tyr Leu Gly Cys Gln Ser Trp Thr Cys Pro Tyr Thr Gly Ala Val
     115                 120                 125

Ser Ser Pro Tyr Trp Lys Phe Gln Gln Asp Val Asn Phe Thr Gln Glu
     130                 135                 140

Val Ser Arg Leu Asn Ile Asn Leu His Phe Ser Lys Cys Gly Phe Pro
145                 150                 155                 160

Phe Ser Leu Leu Val Asp Ala Pro Gly Tyr Asp Pro Ile Trp Phe Leu
                 165                 170                 175

Asn Thr Glu Pro Ser Gln Leu Pro Pro Thr Ala Pro Pro Leu Leu Pro
              180                 185                 190

His Ser Asn Leu Asp His Ile Leu Glu Pro Ser Ile Pro Trp Lys Ser
              195                 200                 205

Lys Leu Leu Thr Leu Val Gln Leu Thr Leu Gln Ser Thr Asn Tyr Thr
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        210                  215                     220

Cys Ile Val Cys Ile Asp Arg Ala Ser Leu Ser Thr Trp His Val Leu
225                 230                 235                     240

Tyr Ser Pro Asn Val Ser Val Pro Ser Ser Ser Ser Thr Pro Leu Leu
                245                 250                     255

Tyr Pro Ser Leu Ala Leu Pro Ala Pro His Leu Thr Leu Pro Phe Asn
                260                 265                 270

Trp Thr His Cys Phe Asp Pro Gln Ile Gln Ala Ile Val Ser Ser Pro
        275                 280
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